

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/519,812
Source: PCT/10
Date Processed by STIC: 1/12/05

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/519,812

DATE: 01/12/2005

TIME: 10:05:30

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\01122005\J519812.raw

3 <110> APPLICANT: Byrne, Barry J.

4 Mah, Cathryn S.

6 <120> TITLE OF INVENTION: rAAV COMPOSITIONS AND METHODS FOR DELIVERY OF HUMAN FACTOR

VII

7 POLYPEPTIDES AND TREATMENT OF HEMOPHILIA A

9 <130> FILE REFERENCE: 4300.014300

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/519,812

12 <141> CURRENT FILING DATE: 2004-12-28

14 <150> PRIOR APPLICATION NUMBER: PCT/US03/20756

15 <151> PRIOR FILING DATE: 2003-06-30

17 <150> PRIOR APPLICATION NUMBER: 60/392,725

18 <151> PRIOR FILING DATE: 2002-06-28

20 <160> NUMBER OF SEQ ID NOS: 17

22 <170> SOFTWARE: PatentIn version 3.2

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 1440

26 <212> TYPE: DNA

27 <213> ORGANISM: Homo sapiens

29 <400> SEQUENCE: 1

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34	gaggagaaac	acgggacatg	ccgttggaaac	cggggctca	cagactcttc	gtaaacccagg	180
36	aggaagccca	cggcgctctg	caccggcgcc	ggcgcccaa	cgcgttctg	gaggagctgc	240
38	ggccgggctc	cctggagagg	gagtgcagg	aggagcagtg	tccttcgag	gaggccccggg	300
40	agatcttcaa	ggacgcggag	aggacgaacg	tgttctggat	ttcttacagt	gatggggacc	360
42	agtgtgcctc	aagtccatgc	cagaatgggg	gctctgcaa	ggaccagctc	cagtctata	420
44	tctgttctg	cctccctgcc	ttcgagggcc	ggaactgtga	gacgcacaag	gatgaccagc	480
46	tgtatgtgt	gaacgagaac	ggcggtgtg	agcagtaactg	cagtgaccac	acggccacca	540
48	agcgctctg	tcgggtccac	gaggggtact	ctctgtggc	agacgggggt	tcctgcacac	600
50	ccacagtta	atatccatgt	ggaaaaatac	ctattctaga	aaaaagaaat	gccagcaaac	660
52	cccaaggccg	aattgtgggg	ggcaaggtgt	gccccaaagg	ggagtgtcca	tggcagggtcc	720
54	tgtgttgggt	gaatggagct	cagttgtgtg	gggggaccc	gatcaacacc	atctgggtgg	780
56	tctccgcggc	ccactgttcc	gacaaaatca	agaactggag	gaacctgatc	gccccgtctgg	840
58	gcgagcacga	cctcagcgag	cacgacgggg	atgagcagag	ccggcggtgt	gcccgggtca	900
60	tcatccccag	cacgtacgtc	ccgggcacca	ccaaccacga	catcgctcg	ctccgcctgc	960
62	accagcccg	ggtcctca	gaccatgtgg	tgcctctg	cctggccgaa	cgacgttct	1020
64	ctgagaggac	gctggcttc	gtgcgttct	cattgtcag	cggtctgggc	cagctgtgg	1080
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68	actgcctgca	gcagtacgg	aagggtggag	actccccaaa	tatcacggag	tacatgttct	1200
70	gtgccggcta	ctcgatggc	agcaaggact	cctgcaaggg	ggacagtgg	ggcccacatg	1260
72	ccacccacta	ccggggcacg	tgttacctga	cgggcatctg	cagctggggc	caggcgtcg	1320
74	caaccgtggg	ccactttggg	gtgtacacca	gggtctccca	gtacatcgag	tggctgcaaa	1380
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81 <212> TYPE: PRT
82 <213> ORGANISM: Homo sapiens
84 <400> SEQUENCE: 2
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91 20 25 30
94 Arg Asp Met Pro Trp Lys Pro Gly Pro His Arg Val Phe Val Thr Gln
95 35 40 45
98 Glu Glu Ala His Gly Val Leu His Arg Arg Arg Arg Ala Asn Ala Phe
99 50 55 60
102 Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu
103 65 70 75 80
106 Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
107 85 90 95
110 Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser
111 100 105 110
114 Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr
115 115 120 125
118 Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His
119 130 135 140
122 Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln
123 145 150 155 160
126 Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu
127 165 170 175
130 Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu
131 180 185 190
134 Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
135 195 200 205
138 Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys
139 210 215 220
142 Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly
143 225 230 235 240
146 Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His Cys Phe Asp
147 245 250 255
150 Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His Asp
151 260 265 270
154 Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val
155 275 280 285
158 Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala
159 290 295 300
162 Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro
163 305 310 315 320
166 Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val
167 325 330 335
170 Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala
171 340 345 350
174 Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu Met Thr Gln

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178	Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser	Pro	Asn Ile Thr	
179	370	375	380	
182	Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser	Lys Asp Ser Cys		
183	385	390	395	400
186	Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr Trp			
187	405	410	415	
190	Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly			
191	420	425	430	
194	His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln			
195	435	440	445	
198	Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro			
199	450	455	460	
202	Phe Pro			
203	465			
206	<210> SEQ ID NO: 3			
207	<211> LENGTH: 1401			
208	<212> TYPE: DNA			
209	<213> ORGANISM: Homo sapiens			
211	<400> SEQUENCE: 3			
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214	gcaggcgggg tcgctaaggc ctcaggagga gaaacacggg acatgcgtg gaagccgggg		120	
216	cctcacagag tcttcgtAAC ccaggagggaa gccacacggc tcctgcaccg gcgcggcgc		180	
218	gccaacgcgt tcctggagga gctgcggccg ggctccctgg agagggagtg caaggaggag		240	
220	cagtgccttc tcgaggaggc ccgggagatc ttcaaggacg cggagaggac gaagctgttc		300	
222	tggatttctt acagtgtatgg ggaccagtgt gcctcaagtc catgccagaa tgggggtctcc		360	
224	tgcaaggacc agctccagtc ctatatctgc ttctgcctcc ctgccttcga gggccggaac		420	
226	tgtgagacgc acaaggatga ccagctgatc tttgtgaaacg agaacggccg ctgtgacgag		480	
228	tactgcgtg accacacggg caccaagcgc tcctgtcggt gccacgaggg gtactctctg		540	
230	ctggcagacg ggggtgcctg cacacccaca gttaatatc catgtggaaa aatacctatt		600	
232	ctagaaaaaa gaaatgccag caaaccaccaaa ggccgaattt tggggggcaa ggtgtgcccc		660	
234	aaaggggagt gtccatggca gtcctgttg ttgggtatg gagctcagtt gtgtgggggg		720	
236	accctgtatca acaccatctg gttgtctcc gcggccact gtttcgacaa aatcaagaac		780	
238	tggaggaacc tgatgcgggt gtcggcgag cacgaccta gcgagcacga cggggatgag		840	
240	cagagccggc ggggtggcgca ggtcatcatc cccagcacgt acgtcccgcc caccaccaac		900	
242	cacgacatcg cgctgcctcg cttgcaccag cccgtggcc tcactgacca tttgtgcccc		960	
244	ctctgcctgc ccgaacggac gttctctgag aggacgctgg ctttcgtgcg ctttcattt		1020	
246	gtcagcggct gggcccgact gtcggaccgt ggcgccacgg ccctggagct catgggtctc		1080	
248	aacgtgcccc ggctgtatgac ccaggactgc ctgcacgt cacggaaatgt gggagactcc		1140	
250	ccaaatatca cggagatcat gttctgtgcc ggctactcgat atggcagacaa ggactcctgc		1200	
252	aagggggaca gtggaggccc acatgccacc cactaccggg gcacgtggta cctgacgggc		1260	
254	atcgctcgt gggcccgagg ctgcgcacc gttggccact ttgggtgtta caccagggtc		1320	
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262	<211> LENGTH: 466			
263	<212> TYPE: PRT			
264	<213> ORGANISM: Homo sapiens			
266	<400> SEQUENCE: 4			

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268 Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
 269 1 5 10 15
 272 Gly Cys Leu Ala Ala Gly Gly Val Ala Lys Ala Ser Gly Gly Glu Thr
 273 20 25 30
 276 Arg Asp Met Pro Trp Lys Pro Gly Pro His Arg Val Phe Val Thr Gln
 277 35 40 45
 280 Glu Glu Ala His Gly Val Leu His Arg Arg Arg Arg Ala Asn Ala Phe
 281 50 55 60
 284 Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu
 285 65 70 75 80
 288 Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
 289 85 90 95
 292 Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser
 293 100 105 110
 296 Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr
 297 115 120 125
 300 Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His
 301 130 135 140
 304 Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln
 305 145 150 155 160
 308 Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu
 309 165 170 175
 312 Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu
 313 180 185 190
 316 Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
 317 195 200 205
 320 Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys
 321 210 215 220
 324 Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly
 325 225 230 235 240
 328 Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His Cys Phe Asp
 329 245 250 255
 332 Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His Asp
 333 260 265 270
 336 Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val
 337 275 280 285
 340 Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala
 341 290 295 300
 344 Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro
 345 305 310 315 320
 348 Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val
 349 325 330 335
 352 Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala
 353 340 345 350
 356 Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu Met Thr Gln
 357 355 360 365
 360 Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro Asn Ile Thr
 361 370 375 380
 364 Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys

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365	385	390	395	400												
368	Lys	Gly	Asp	Ser	Gly	Gly	Pro	His	Ala	Thr	His	Tyr	Arg	Gly	Thr	Trp
369					405					410					415	
372	Tyr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Gln	Gly	Cys	Ala	Thr	Val	Gly
373					420					425					430	
376	His	Phe	Gly	Val	Tyr	Thr	Arg	Val	Ser	Gln	Tyr	Ile	Glu	Trp	Leu	Gln
377					435					440					445	
380	Lys	Leu	Met	Arg	Ser	Glu	Pro	Arg	Pro	Gly	Val	Leu	Leu	Arg	Ala	Pro
381					450					455					460	
384	Phe	Pro														
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